

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/550,584

CRF Edit Date: 10/7/05
Edited by: h

- Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line
- Corrected the SEQ ID NO. Sequence numbers edited were:

1 7

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

7

- Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

- Inserted mandatory headings/numeric identifiers, specifically:

- Moved responses to same line as heading/numeric identifier, specifically:

- Other:



PCT10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/550,584

DATE: 10/07/2005

TIME: 16:33:57

Input Set : A:\PTO.AMC.txt
 Output Set: N:\CRF4\10072005\J550584.raw

3 <110> APPLICANT: SHINOZAKI, Kazuko
 4 KATSURA, Koji
 5 ITO, Yusuke
 7 <120> TITLE OF INVENTION: Stress-inducible promoter and method for using the same
 9 <130> FILE REFERENCE: 382.1048
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/550,584
 C--> 11 <141> CURRENT FILING DATE: 2005-09-22
 11 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/002563
 12 <151> PRIOR FILING DATE: 2004-03-02
 14 <150> PRIOR APPLICATION NUMBER: JP 2003-080847
 15 <151> PRIOR FILING DATE: 2003-03-24
 17 <160> NUMBER OF SEQ ID NOS: 12
 19 <170> SOFTWARE: PatentIn Ver. 2.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1066
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Oryza sativa
 26 <220> FEATURE:
 27 <223> OTHER INFORMATION: Inventor: Shinozaki, Kazuko; Katsura, Koji; Ito, Yusuke
 29 <400> SEQUENCE: 1
 30 tcatcagcta tcataaaggc gaaggaaaaga aagaaaaata aaaggaaaag aactggctgg 60
 31 aaatttagaga agccccggac gactcgatct ggggggtggca attaatcag tgtgatcaac 120
 32 agggataact tatcccgtcc gaccaaattcc accaaccaaa ccaagaccgg attttttagg 180
 33 ctgtgaaaga cggatcagtg ggaccctgat ctacggaccc catatgtcac cgccgggtc 240
 34 tctggatctc tcccggtcgcc ctaatcagac accgcgcgcg cgggtggccgtc gctctcgagc 300
 35 cgtgtcccgcc tcccaactcg tcacaaaaggc gatcacagac tcttccttcc tctgctggga 360
 36 gagaagaaaa attggccgcg atgatgccga taaagaggaa aaaggatgaa gaatccgatg 420
 37 gaaaaaaact gatgttaatc tatcgactact gctgcgcact aagacgaatc gtatccgaac 480
 38 aagaaacgct tacgttactg ttccctaaatg gatcgctccg ctcatcactt aacccaaaat 540
 39 cgatttaggaa attgacggac agcgacgccc gaagccaagt gtctcggtcg gtggcggtc 600
 40 aggccctcgaa gcagaggggag cggagaggcg gacgcgcgcg ccacgcctcc tctccctcg 660
 41 tgacacggcc gtctggctcc acatggcgcc gacccctccc gatgcgtcca cccgtcccg 720
 42 ggacccgcca cgtcggaaacc agccggccgc cccacgcgt tgccgacacg cgtcgccgc 780
 43 ccactggctc acccgctgccc tgccctgtcc tgccccccat ctcgtcgcca tttcccgccc 840
 44 acgttcttg tcctcggtc gcctacgcgt acgtacgata caaacgccc acctttcgat 900
 45 cccctccgct atataaggag ggcattgtcc tcgccccctt cttcatccga aagaaaaaggc 960
 46 gactcggtcac agctcaaaca agtcaagagc gaatagttct tgctgatctg ttgtttgatt 1020
 47 acttttagttc tcgagaggct ttagctgaat ccatcgatcg aggatg 1066
 50 <210> SEQ ID NO: 2
 51 <211> LENGTH: 1245
 52 <212> TYPE: DNA
 53 <213> ORGANISM: Oryza sativa
 55 <400> SEQUENCE: 2

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Input Set : A:\PTO.AMC.txt
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56 gctagcagag ctcgtcacag ctcaaacaag tcaagagcga atagttcttg ctgatctgtt 60
 57 gttgattac tttagttctc gagaggctt agctgaatcc atcgatcgat catggaggat 120
 58 gagaggaaca cggagagcca ccagggtggc gaggctgcag agcaggtgga ggtgaaggac 180
 59 aggggcctt tcgacaacct ccttggcagg aagaaggacg atcagccgga ggagaagaag 240
 60 catgaggagg agcttgcac cgcatggag aaggtctccg tggaaagagcc aaagaaggag 300
 61 gaggcaccacg ccgagggcga gaagaaggag agcctctt ccaagctgca ccgatccagc 360
 62 tccagctcca gtcgtcgag ttagtggagaa gaggaggtga tcgatgacaa cggcgaggtg 420
 63 gtcaagagga agaagaagaa ggggctcaag gagaagatca aggagaagct gcccggccac 480
 64 aaggaccatg ccggtgagca tgctctccg cccgcggcga cgggcttccc ggcggccgtc 540
 65 cgctgcattcc gtggtgacgg ccgcgcacccac gccactcctg ctccctgtt gactcacggc 600
 66 gatcaccacc acgacaccgc cgtccccgtg gaaaagatcg agggtgatca cgccagacgg 660
 67 agggcaccct gccacgtgca cccgaggagg aaaaaaggcc ttccctcgaca agatcaagga 720
 68 gaagctgccc ggcggccaca agaagccgga agacgcaact gctgtccgc cgcggccgc 780
 69 ctaccggct gtcctgcca ctactccggc gccagcacac ccaccggccgg ctacagagga 840
 70 agtgagcagc ccggatggga aggagaagaa gggtatactg ggcaagatca tggagaaact 900
 71 gcccggttac cacaagggtc ccggcgagga agacaagacc gccgcgcgc ccaccggcga 960
 72 gcacaagagc agcgcttaat tggggcgtgt gtgagaccag gccatggttt gaatttggaa 1020
 73 gtgttggcg tggtagtt tggtagttt tctgcactgc agctttgtt agttcgtgtc 1080
 74 aagattggtc aaggcctggt cagcgaagcc cgatcagtga tcaagttt tgttcgtgt 1140
 75 ggggtacggg cttcagttt ctatagtca gtactagatg ttgagttt ttaatttattta 1200
 76 ttggcactt tggatgggtt ttggctggg cattctgcct tggta 1245
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 80 <211> LENGTH: 28
 81 <212> TYPE: DNA
 82 <213> ORGANISM: Artificial Sequence
 84 <220> FEATURE:
 85 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
 87 <400> SEQUENCE: 3
 88 cacgaagctt tcatacgacta ttcatcaa 28
 91 <210> SEQ ID NO: 4
 92 <211> LENGTH: 28
 93 <212> TYPE: DNA
 94 <213> ORGANISM: Artificial Sequence
 96 <220> FEATURE:
 97 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
 99 <400> SEQUENCE: 4
 100 ccggatccctc gatcgatggaa ttcaagcta 28
 103 <210> SEQ ID NO: 5
 104 <211> LENGTH: 1608
 105 <212> TYPE: DNA
 106 <213> ORGANISM: Oryza sativa
 108 <400> SEQUENCE: 5
 109 caacaaccac tactgaacac ggctaagtgt gttcctctc ctcgaagatg tcgttattgc 60
 110 gttttttct gctattccat acatataat ctctagagga acaccttact ctatgtttca 120
 111 gacaagggac ggtggtaaat cacgtcgat cctccatggg gtgtctccg aaaaaccttc 180
 112 cctcatgcat tagagatcat gggatggatt tagcgatggc acaccttatt tataatttag 240
 113 ttactctccg gcggtaccat ctgcttcgt ttgttgcgt atgcggcga tgatgtgt 300
 114 gagtatacgat caacagaatg atcggacgtt attttgggg tcgtttttt tcagcattga 360
 115 ggagggatga ggattgcttg caacatgcag gtgctgctca aaacaacgggtaaagcagata 420

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116 tccgtcaatt tgatagtaag atctgttaacg cgtggcttt cgagctgaaa actatggact 480
117 ctttgaaca aagataaat tatattaaat tctattattc aaagatatct aaatatttag 540
118 aaagatatta ataatgttat taaaactttaa cttacttaaa acaagtccaa aactgcatgt 600
119 ccctaaatcg ccagaagata aggaacacct gtaccgtga taacagaggg gtatgaaatt 660
120 tggacacgag gcttcttgg cagacgtggc gctgagttag cttggctcg ttgtcaaac 720
121 tccgtgcagg gacattcagt tagctagcta gcagcattgt cgacaataag atagcctta 780
122 aatgttagca ctcaccagct tgtaaaaaac caaggcttgg tgacggccgc ttcaaatga 840
123 aggatagatg gataaatgtc tagaatattt taaagtccaa caaaagatgg agcacatgca 900
124 tggaaagatta cgtacacgaa tgcagttgtat acagtggatg ttaggcataa gaagcactat 960
125 aaatagaggg tgcaatcccc attgcccctac acaactacac aagtcgacta tcattacaag 1020
126 gaaatttaaag cgaccacgaa ggtatgaaag catagcagta ctctgcattt ttttttttg 1080
127 atgttggctc agctagctc gcttaaggtt ttccttctt tcgttcttg tttttttttt 1140
128 gtaagctcaa cttagtgcattt gcaatttaga ttttacattt ttacagttgg aaaaacatcc 1200
129 ctataaaatata taccatgaat gcatagagat tcgaggaagc tacaatatttgg acgactgatt 1260
130 ccaaaaaaaaaaaaaaaaatc agatggtcac atcattgcta ttgttttgg aaagtacaaa 1320
131 agcaactcggtt cggattcaaa ttacttgc 1380
132 gtaccccta cacattcgg aaacaatacc atatatgtta gtgtgcgatc attcaatttgc 1440
133 atttatatctt gaacaaaact gaggggat acggtagca aacttgacga ttccaaaata 1500
134 atttatattt aggcaaaattt ttacaacttc aaagttcaaa caagctaacc tgaaaaatca 1560
135 tggttgaatt tactaagatg tgctttgtt tttactaaac agagtatg 1608

138 <210> SEQ ID NO: 6

139 <211> LENGTH: 927

140 <212> TYPE: DNA

141 <213> ORGANISM: Oryza sativa

143 <220> FEATURE:

144 <221> NAME/KEY: CDS

145 <222> LOCATION: (69)..(782)

147 <400> SEQUENCE: 6

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150 atccgaag atg tgc ggg atc aag cag gag atg agc ggc gag tcg tcg ggg 110
151 Met Cys Gly Ile Lys Gln Glu Met Ser Gly Glu Ser Ser Gly
152 1 5 10
154 tcg ccg tgc agc tcg gcg tcg gag cgg cag cac cag acg gtg tgg 158
155 Ser Pro Cys Ser Ser Ala Ser Ala Glu Arg Gln His Gln Thr Val Trp
156 15 20 25 30
158 acg gcg ccg aag agg ccg gcg ggg cgg acc aag ttc agg gag acg 206
159 Thr Ala Pro Pro Lys Arg Pro Ala Gly Arg Thr Lys Phe Arg Glu Thr
160 35 40 45
162 agg cac ccg gtg ttc cgc ggc gtg cgg cgg agg ggc aat gcc ggg agg 254
163 Arg His Pro Val Phe Arg Gly Val Arg Arg Gly Asn Ala Gly Arg
164 50 55 60
166 tgg gtg tgc gag gtg cgg gtg ccc ggg cgg cgc ggc tgc agg ctc tgg 302
167 Trp Val Cys Glu Val Arg Val Pro Gly Arg Arg Gly Cys Arg Leu Trp
168 65 70 75
170 ctc ggc acg ttc gac acc gcc gag ggc gcg ggc cgc ggc cac gac gcc 350
171 Leu Gly Thr Phe Asp Thr Ala Glu Gly Ala Ala Arg Ala His Asp Ala
172 80 85 90
174 gcc atg ctc gcc atc aac gcc ggc ggc ggc ggc ggg gga gca tgc 398
175 Ala Met Leu Ala Ile Asn Ala Gly Gly Gly Gly Gly Ala Cys

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176	95	100	105	110														
178	tgc	ctc	aac	ttc	gcc	gac	tcc	gcg	tgg	ctc	ctc	gcc	gtg	ccg	cgc	tcc	446	
179	Cys	Leu	Asn	Phe	Ala	Asp	Ser	Ala	Trp	Leu	Leu	Ala	Val	Pro	Arg	Ser		
180																125		
182	tac	cgc	acc	ctt	cgc	cga	cgt	ccg	cca	cgc	cgt	gcc	gag	gcc	gtc	gag	494	
183	Tyr	Arg	Thr	Leu	Arg	Arg	Arg	Pro	Pro	Arg	Arg	Ala	Glu	Ala	Val	Glu		
184																140		
186	gac	ttc	ttc	cg	cg	cg	ct	cc	gac	gac	g	ct	tg	tcc	gcc	ac	tcg	542
187	Asp	Phe	Arg	Arg	Arg	Leu	Ala	Asp	Asp	Ala	Leu	Ser	Ala	Thr	Ser			
188																155		
190	tcg	tcc	tcg	ac	cg	cc	ttc	cc	cg	cc	ac	gac	gac	gac	gag	gag	590	
191	Ser	Ser	Ser	Thr	Thr	Pro	Ser	Thr	Pro	Arg	Thr	Asp	Asp	Asp	Glu	Glu		
192																170		
195	tcc	gcc	gcc	acc	gac	ggc	gac	gag	tcc	tcc	tcc	ccg	gcc	ac	gac	ctg	638	
196	Ser	Ala	Ala	Thr	Asp	Gly	Asp	Glu	Ser	Ser	Ser	Pro	Ala	Ser	Asp	Leu		
197	175															190		
199	g	cg	ttc	gaa	ctg	gac	gtc	ctg	agt	gac	atg	ggc	tgg	gac	ctg	tac	686	
200	Ala	Phe	Glu	Leu	Asp	Val	Leu	Ser	Asp	Met	Gly	Trp	Asp	Leu	Tyr	Tyr		
201																205		
203	g	cg	ag	tt	g	cg	c	g	gg	at	g	cc	cc	tc	g	cg	734	
204	Ala	Ser	Leu	Ala	Gln	Gly	Met	Leu	Met	Glu	Pro	Pro	Ser	Ala	Ala	Leu		
205																220		
207	gg	g	ac	g	gg	at	cc	tc	g	cc	tc	tgg	ag	tc	ac	782		
208	Gly	Asp	Asp	Gly	Asp	Ala	Ile	Leu	Ala	Asp	Val	Pro	Leu	Trp	Ser	Tyr		
209																235		
211	tag	ag	ctt	aa	t	ttt	tt	842										
212	caaa	at	ttt	tg	gt	act	gt	ac	tt	tc	gg	ta	at	gt	gg	aa	902	
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216	<210>	SEQ	ID	NO:	7													
217	<211>	LENGTH:	1437															
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222	<221>	NAME/KEY:	CDS															
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227	g	a	t	a	c	a	c	g	a	g	t	t	c	g	a	g	120	
228	t	t	t	c	a	a	t	t	g	t	g	g	a	g	g	at	175	
229																Met	Ala	Val
230																1		
231	t	a	t	g	a	g	t	a	g	a	c	a	ca	tt	g	at	223	
232	Tyr	Asp	Gln	Ser	Gly	Asp	Arg	Asn	Arg	Thr	Gln	Ile	Asp	Thr	Ser	Arg		
233																		
234	aaa	agg	aaa	tct	aga	agt	aga	ggt	gac	ggt	act	act	gt	g	ct	gag	aga	271
235	Lys	Arg	Lys	Ser	Arg	Ser	Arg	Gly	Asp	Gly	Thr	Thr	Val	Ala	Glu	Arg		
236																		
237	tta	aag	aga	tgg	aaa	gag	tat	aac	gag	acc	gta	gaa	gaa	gtt	tct	acc	319	
238	Leu	Lys	Arg	Trp	Lys	Glu	Tyr	Asn	Glu	Thr	Val	Glu	Glu	Val	Ser	Thr		

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240	aag aag agg aaa gta cct gcg aaa ggg tcg aag aag ggt tgt atg aaa			367
241	Lys Lys Arg Lys Val Pro Ala Lys Gly Ser Lys Lys Gly Cys Met Lys			
242	55	60	65	
243	ggt aaa gga gga cca gag aat agc cga tgt agt ttc aga gga gtt agg			415
244	Gly Lys Gly Gly Pro Glu Asn Ser Arg Cys Ser Phe Arg Gly Val Arg			
245	70	75	80	
246	caa agg att tgg ggt aaa tgg gtt gct gag atc aga gag cct aat cga			463
247	Gln Arg Ile Trp Gly Lys Trp Val Ala Glu Ile Arg Glu Pro Asn Arg			
248	85	90	95	
249	ggt agc agg ctt tgg ctt ggt act ttc cct act gct caa gaa gct gct			511
250	Gly Ser Arg Leu Trp Leu Gly Thr Phe Pro Thr Ala Gln Glu Ala Ala			
251	100	105	110	115
252	tct gct tat gat gag gct gct aaa gct atg tat ggt cct ttg gct cgt			559
253	Ser Ala Tyr Asp Glu Ala Ala Lys Ala Met Tyr Gly Pro Leu Ala Arg			
254	120	125	130	
255	ctt aat ttc cct cgg tct gat gcg tct gag gtt acg agt acc tca agt			607
256	Leu Asn Phe Pro Arg Ser Asp Ala Ser Glu Val Thr Ser Thr Ser			
257	135	140	145	
258	cag tct gag gtg tgt act gtt gag act cct ggt tgt gtt cat gtg aaa			655
259	Gln Ser Glu Val Cys Thr Val Glu Thr Pro Gly Cys Val His Val Lys			
260	150	155	160	
261	aca gag gat cca gat tgt gaa tct aaa ccc ttc tcc ggt gga gtg gag			703
262	Thr Glu Asp Pro Asp Cys Glu Ser Lys Pro Phe Ser Gly Gly Val Glu			
263	165	170	175	
264	ccg atg tat tgt ctg gag aat ggt gcg gaa gag atg aag aga ggt gtt			751
265	Pro Met Tyr Cys Leu Glu Asn Gly Ala Glu Glu Met Lys Arg Gly Val			
266	180	185	190	195
267	aaa gcg gat aag cat tgg ctg agc gag ttt gaa cat aac tat tgg agt			799
268	Lys Ala Asp Lys His Trp Leu Ser Glu Phe Glu His Asn Tyr Trp Ser			
269	200	205	210	
270	gat att ctg aaa gag aaa gag aag gag caa ggg att gta gaa			847
271	Asp Ile Leu Lys Glu Lys Glu Lys Gln Lys Glu Gln Gly Ile Val Glu			
272	215	220	225	
273	acc tgt cag caa caa cag cag gat tcg cta tct gtt gca gac tat ggt			895
274	Thr Cys Gln Gln Gln Gln Asp Ser Leu Ser Val Ala Asp Tyr Gly			
275	230	235	240	
276	tgg ccc aat gat gtg gat cag agt cac ttg gat tct tca gac atg ttt			943
277	Trp Pro Asn Asp Val Asp Gln Ser His Leu Asp Ser Ser Asp Met Phe			
278	245	250	255	
279	gat gtc gat gag ctt cta cgt gac cta aat ggc gac gat gtg ttt gca			991
280	Asp Val Asp Glu Leu Leu Arg Asp Leu Asn Gly Asp Asp Val Phe Ala			
281	260	265	270	275
282	ggc tta aat cag gac cgg tac ccg ggg aac agt gtt gcc aac ggt tca			
283	Gly Leu Asn Gln Asp Arg Tyr Pro Gly Asn Ser Val Ala Asn Gly Ser			
284	280	285	290	
285	tac agg ccc gag agt caa caa agt ggt ttt gat ccg cta caa agc ctc			1087
286	Tyr Arg Pro Glu Ser Gln Gln Ser Gly Phe Asp Pro Leu Gln Ser Leu			
287	295	300	305	

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/550,584

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\10072005\J550584.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:148 M:112 C: (48) String data converted to lower case,

M:112 Repeated in SeqNo=6